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PCT09

## RAW SEQUENCE LISTING

DATE: 11/01/2001

PATENT APPLICATION: US/09/700,813

TIME: 09:59:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\11012001\I700813.raw

3 <110> APPLICANT: SIERRA-HONIGMANN, Rocio  
5 <120> TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND WOUND HEALING  
7 <130> FILE REFERENCE: 044574-5029  
9 <140> CURRENT APPLICATION NUMBER: US 09/700,813  
10 <141> CURRENT FILING DATE: 1999-05-20  
12 <150> PRIOR APPLICATION NUMBER: PCT/US99/11209  
13 <151> PRIOR FILING DATE: 1999-05-20  
15 <150> PRIOR APPLICATION NUMBER: US 60/086,354  
16 <151> PRIOR FILING DATE: 1998-05-28  
18 <160> NUMBER OF SEQ ID NOS: 21  
20 <170> SOFTWARE: PatentIn version 3.0  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 3656  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Mus musculus  
27 <400> SEQUENCE: 1

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38	ttcaagtggg	atctacgttc	ctgagttatc	caaaacagtc	ttccactgtt	gctttgggaa	360
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153 <212> TYPE: PRT
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162 20 25 30
164 Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
165 35 40 45
167 Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
168 50 55 60
170 Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
171 65 70 75 80
173 Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
174 85 90 95
176 Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
177 100 105 110

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179 Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
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182 Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Ile Ile Cys His Met
183      130      135      140
185 Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
186 145      150      155      160
188 Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
189      165      170      175
191 Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
192      180      185      190
194 Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
195      195      200      205
197 Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
198      210      215      220
200 Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
201 225      230      235      240
203 Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
204      245      250      255
206 Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
207      260      265      270
209 Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
210      275      280      285
212 Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
213      290      295      300
215 Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
216 305      310      315      320
218 Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
219      325      330      335
221 Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
222      340      345      350
224 Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
225      355      360      365
227 Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
228      370      375      380
230 Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
231 385      390      395      400
233 Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
234      405      410      415
236 His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
237      420      425      430
239 Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
240      435      440      445
242 Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
243      450      455      460
245 His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
246 465      470      475      480
248 Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
249      485      490      495
251 Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg

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255				515				520				525		
257	Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys
258				530				535				540		
260	Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys
261	545					550					555			560
263	Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu
264						565					570			575
266	Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys
267				580					585					590
269	Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val
270				595				600					605	
272	Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn
273				610				615				620		
275	Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met
276	625					630					635			640
278	Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys
279						645					650			655
281	Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser
282				660							665			670
284	Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn
285				675				680				685		
287	Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu
288				690				695				700		
290	Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu
291	705					710					715			720
293	Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser
294						725					730			735
296	Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser
297				740					745					750
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300				755					760					765
302	Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys
303				770					775			780		
305	Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn
306	785					790					795			800
308	Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met
309						805					810			815
311	Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala
312				820					825					830
314	Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile
315				835					840					845
317	Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His
318				850					855					860
320	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn
321	865					870					875			880
323	Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu
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330          915          920          925
332 Lys Asp Glu Met Val Pro Ala Ala Met Val Ser Leu Leu Leu Thr Thr
333          930          935          940
335 Pro Asp Pro Glu Ser Ser Ser Ile Cys Ile Ser Asp Gln Cys Asn Ser
336 945          950          955          960
338 Ala Asn Phe Ser Gly Ser Gln Ser Thr Gln Val Thr Cys Glu Asp Glu
339          965          970          975
341 Cys Gln Arg Gln Pro Ser Val Lys Tyr Ala Thr Leu Val Ser Asn Asp
342          980          985          990
344 Lys Leu Val Glu Thr Asp Glu Glu Gln Gly Phe Ile His Ser Pro Val
345          995          1000          1005
347 Ser Asn Cys Ile Ser Ser Asn His Ser Pro Leu Arg Gln Ser Phe
348          1010          1015          1020
350 Ser Ser Ser Ser Trp Glu Thr Glu Ala Gln Thr Phe Phe Leu Leu
351          1025          1030          1035
353 Ser Asp Gln Gln Pro Thr Met Ile Ser Pro Gln Leu Ser Phe Ser
354          1040          1045          1050
356 Gly Leu Asp Glu Leu Leu Glu Leu Glu Gly Ser Phe Pro Glu Glu
357          1055          1060          1065
359 Asn His Arg Glu Lys Ser Val Cys Tyr Leu Gly Val Thr Ser Val
360          1070          1075          1080
362 Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly Glu Ala Gly Ile
363          1085          1090          1095
365 Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp Ile Arg Ile
366          1100          1105          1110
368 Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu Ser Leu
369          1115          1120          1125
371 Gly Thr Ser Gly Glu Asn Phe Val Pro Tyr Met Pro Gln Phe Gln
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381 <211> LENGTH: 539
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383 <213> ORGANISM: Rattus norvegicus
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390 ccaaaaccct catcaagacc attgtcacca ggatcaatga catttcacac acgcagtcgg      180
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396 cccaaaacgt gctgcagata gctcatgacc tggagaacct gcgagacctc ctccatctgc      360
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VERIFICATION SUMMARY

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